

New Tools to Meet New Challenges: Emerging Technologies for Managing Marine Ecosystems for Resilience

GRETCHEN E. HOFMANN AND STEVEN D. GAINES

The goal of this article is to highlight evolving tools, recent advances, and emerging techniques that are being used to understand natural variability in marine ecosystems. These technical approaches range from the tagging of large pelagic organisms to the use of genomics to provide insight into the abundance and health of marine organisms. Although these techniques vary dramatically in scale, they share the potential to remove critical impediments to the effective management of marine systems.

Keywords: marine ecosystem-based management, marine ecosystems, resilience

As the momentum for the study of ecosystem resiliency increases, more data are critically needed about the members of the ecosystems under study. Ironically, ecosystem-based management places even greater demands on the study of individual organisms because of the need for simultaneous information on multiple species. Specifically, what species are present or absent? What are their distributions across their geographic ranges? And what is the physiological health of organisms in these natural populations? Although most of this information can be estimated, the need for accurate data about organisms in nature is essential to understanding how an ecosystem is responding to perturbations and how it might rebound from disturbance. Thus, the emergence of ecosystem-based management, coupled with increased awareness of human impacts on ecosystems, has driven the need for organismal data that have greater resolution and accuracy. Not surprisingly, anytime a new way of doing science emerges, new bottlenecks to progress arise. And, in such research-driven fields, conceptual advances often drive technological advances targeted at breaking these bottlenecks. In this article, we provide an entrée to some of the new tools that are available to ecologists studying ecosystems in action.

What species are present?

Because species identification is central to biological research and is especially critical for managers of complex ecosys-

tems, it is essential to develop uniform identification tools. Here, we discuss technologies that are used today to determine what species are present in marine ecosystems.

DNA barcoding. One emerging technique is DNA barcoding, a process whereby a DNA sequence is compiled from a uniform location in the genome, and a “barcode” is generated to uniquely identify a species. Just as a Universal Product Code identifies specific grocery items, biological DNA barcodes can identify living organisms to the species level (Savolainen et al. 2005). Such a universal identification system would be especially useful to managers in situations where a particular kind of taxonomic expertise is not always available and misidentification of organisms becomes a potential problem in biodiversity reports.

Although other DNA or RNA sequencing methods have been established, DNA barcoding is emerging as a preferred technique to develop databases. DNA barcoding has been used successfully to identify varied animal groups to the species level by using the sequence of a mitochondrial gene, cytochrome *c* oxidase subunit I (COI) (Hebert et al. 2003). Initially, DNA barcoding was ground-truthed (corroborated) in two sig-

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nificant studies of biodiversity: combined with traditional taxonomic data, DNA barcoding revealed hidden biodiversity in skipper butterflies from Costa Rica (Hebert et al. 2004) and provided new insight into the diversity of North American birds (Kerr et al. 2007). In marine systems, barcoding has been used to identify species of such diverse taxa as marine fish, invertebrates, phytoplankton, and microbes. Overall, the promise of DNA barcoding is significant from a management perspective: the technique allows for rapid identification; it does not require personnel to have extensive systematic or taxonomic knowledge; and it can identify species at different life-history stages, or variants that cannot be easily separated by eye. Efforts are under way to produce a handheld sequencer that will make DNA barcoding easier in the field, making this technique even more attractive to field biologists.

However, DNA barcoding is not without its problems, and it has been the source of some controversy. DNA taxonomy, the idea that a species can be identified solely by DNA sequence, poses this question: at what point does sequence variation become a taxon? This is not a simple concept, and it relies heavily on molecular systematics and specific bioinformatics tools. The criticisms of the technique fall into two general categories: first, COI sequence differences may not be great enough to distinguish closely related species; second, it is very difficult to tell when a DNA barcode result would misclassify an organism, possibly making barcoding's purported advantages—speed and efficiency via high throughput—a serious disadvantage.

Still, despite controversial aspects, DNA barcoding has advanced within the scientific community, and it stands to make contributions to ecosystem management as groups such as the Consortium for the Barcode of Life (CBOL; www.barcoding.si.edu) become increasingly active. CBOL plans to compile a DNA barcode database for plants and animals that would be available to academics, ecosystem managers, and the public. Cooperative efforts within CBOL include projects to catalog groups of organisms that have significant utility for the management of living resources (e.g., the International Network for Barcoding Invasive and Pest Species [<http://barcoding.si.edu/INBIPS.htm>] and the Fish Barcode of Life Initiative, or FISH-BOL [www.fishbol.org], a project seeking to barcode more than 30,000 marine and freshwater fish species). In addition, resources in this area have expanded with the opening of the Barcode of Life Data Systems Web site (www.barcodinglife.org; Ratnasingham and Hebert 2007). In a similar trend, DNA barcoding strategies are being advocated by consortia interested in conservation biology and biodiversity in marine ecosystems (e.g., the Census of Marine Life [www.coreocean.org/Dev2Go.web?id=255158]). Overall, DNA barcoding can be an important tool for managers who employ conservation genetics.

Ecogenomics in the oceans: Revolutionizing our view of microbial diversity. Of the fields that investigate what species are present in marine environments, none is more cutting-edge than ecogenomics (also called metagenomics), the study of

genetic material recovered directly from environmental samples. In particular, scientists are applying genomic technologies to search for the genomes of as-yet unidentified microbes in samples from the environment (DeLong and Karl 2005). These methods have revolutionized scientists' perspectives on microbial communities and their role in ecosystems, especially with respect to microbial community diversity and metabolic function. Stated simply, the use of whole-genome shotgun sequencing methods to search for microbes in environmental samples is revealing that researchers have greatly underestimated the numbers of species in any one environment and thus, it can be argued, have failed to understand the function of the ecosystem. Although still a somewhat controversial approach to obtaining DNA sequences, whole-genome shotgun sequencing of samples from the marine environment has recently revealed an unprecedented view of microbial diversity in the ocean. In a study in the Sargasso Sea, Craig Venter and colleagues (2004) discovered more than 1.2 million new genes that were derived from an estimated 1800 new microbes. Given the central role that microbes play in functioning ecosystems, ecogenomics has enormous implications for scientists' understanding of diversity in the oceanic microbial community (Eisen 2007), and can also shed significant light on the health of ecosystems if the assemblage of microbes and their functions are eventually understood and mapped onto their geographic locations.

Remote sensing. Satellite and aerial surveys have contributed enormously to the characterization of marine ecosystems by providing tools to survey organisms from afar over large spatial scales. The pace of technological advancement in these remote assessments is far too rapid for even a cursory review of the technology in this article. The biggest hurdles to obtaining useful windows on the spatial and temporal patterns of species abundance, diversity, and productivity in coastal habitats have historically been limits on the level of taxonomic resolution achievable, difficulties with spatial resolution, and complications inherent in surveying coastal habitats (e.g., tides, fog, suspended sediments). These barriers are breaking down as new technologies and analytical approaches expand the range of situations where reliable taxon-specific data are attainable (Kerr and Ostrovsky 2003, Malthus and Mumby 2003). The most noteworthy advances have come in surveys of coral reefs, mangroves (Wang et al. 2004), kelp and algal beds (Guichard et al. 2000, Reed et al. 2006), and estuaries. Higher-resolution, hyperspectral imagers, combined with new analytical approaches, are creating opportunities to use remote monitoring of population size, biodiversity, and individuals' physiological health to inform ecosystem management decisions.

Observatories. Moored and towed instruments have been the staples of ocean monitoring, and especially for monitoring its physical parameters. With the advent of broad arrays of instrumentation in observatories (e.g., Rutgers's LEO-15 [Long-term Ecosystem Observatory; www.marine.rutgers].

edu/mrs/LEO/LEO15.html] and the University of Washington's NEPTUNE system on the Juan de Fuca plate [www.neptune.washington.edu]), cabled instruments with high bandwidth, and the rapid development of autonomous vehicles, *in situ* monitoring of ocean ecosystems is on the cusp of a revolution. Yet the potential benefits of these advances in ocean observation for ecosystem management are constrained because existing instrumentation can effectively monitor only a limited range of biological components of marine ecosystems. Video coupled with real-time image analysis is effective for surveying some components of marine ecosystems (Dennett et al. 2002), and *in situ* DNA analyses (Scholin et al. forthcoming) offer the promise of species-specific sampling.

Connectivity. Managing something requires knowing where it is. Ecosystems are no exception. Regardless of the goals, the success of managing an ecosystem will most likely depend in no small part on defining the ecosystem's bounds. Managing a small subset of an ecosystem without understanding its connections with unmanaged pieces is a recipe for failure (Gaines et al. 2007). Similarly, managing at too large a spatial scale without recognizing the functionally independent ecosystem units poses equally daunting challenges (Siegel et al. 2003, Kinlan et al. 2005). Actions taken at the large scale will be successful only if there is a generic solution that works across ecosystem subunits—a supposition that is rarely justifiable.

Superficially, defining the bounds to an ecosystem may seem to be simply an exercise in mapping habitats. In the coastal ocean, the boundaries of rocky reefs, tidal zones, canyons, estuaries, and many other habitats are often easily identified and mapped (McRea et al. 1999, Greene et al. 2000, Rhoads 2001, Pickrill 2003). Yet even a perfect habitat map of a coastline would provide only limited insight into the relevant boundaries of ecosystems. The problem is that habitat distributions alone may reveal little about patterns of movement. The nature of marine life cycles, and of the fluid medium in which they play out, creates a disproportionately large role for movement in coastal ecosystems (Cowen et al. 2006, Gaines et al. 2007). Currents subsidize local food webs by delivering nutrients and plankton from elsewhere (Broitman et al. 2001, Menge et al. 2003); adult fish, and some invertebrates, can swim enormous distances; and the young of nearly all fish, and the majority of invertebrates, drift as larvae in the plankton, often traveling far from their natal site (Kinlan and Gaines 2003, Gerber et al. 2005, Shanks et al. 2005, Cowen et al. 2006).

Some of the mobile components of coastal ecosystems can now be routinely monitored either from space or through *in situ* instruments. For example, researchers have made enormous advances in understanding the spatial patterns and temporal dynamics of phytoplankton and some nutrients through the repeated mapping of ocean color and temperature (Thomas et al. 2001, Broitman and Kinlan 2005). Because these constituents provide the fuel for productivity in coastal

food webs, the success of ecosystem-based management is tied to understanding these key ecosystem subsidies. This effort has been buoyed greatly by the emergence of large-scale monitoring programs (e.g., US GLOBEC, or Global Ocean Ecosystems Dynamics [www.usglobec.org]; PISCO, or Partnership for Interdisciplinary Studies of Coastal Oceans [www.piscoweb.org]; and the Census of Marine Life [www.coml.org]), which are poised to grow rapidly with the advent of new ocean observing systems.

A much more challenging roadblock to progress, however, has been the difficulty of tracking the movement of fish and invertebrates—both adults and young. The primary problems are the potential scales of movement (up to hundreds or thousands of kilometers) and the frequently small size of the swimmers (down to tens of microns). Many coastal species are highly mobile as adults, with individuals traversing entire ocean basins. In addition, even species that are completely immobile as adults can exhibit extensive movement through the dispersal of young.

When individuals move, the dynamics of subpopulations at their origins and destinations become linked. If many individuals move, ecosystems in different places are intimately coupled. Without a clear understanding of the scales and rates of connectivity and their variability among species and locations, managing ecosystems for resilience (or nearly any other goal) will be daunting and very likely unsuccessful. For example, the pace of recovery from a disturbance depends on the rate of recolonization (Peterson et al. 1998). If new recruits must arrive from elsewhere, the patterns of connectivity are critical for determining when or if recovery will occur. If many young arrive from distant undisturbed sites, recovery may be rapid. If, on the other hand, recruits are mostly young of local adults, recovery may be slow or nonexistent (Kinlan and Gaines 2003, Kinlan et al. 2005). Similarly, the effects of a disturbance at one location can be transported elsewhere by shutting off the normal delivery of young. Disturbances at a source site could have their largest impacts at distant sites, which now receive fewer young.

Connectivity matters, and ignorance about connectivity constrains the effectiveness of ecosystem-based management (Hastings and Botsford 2006). Disturbances, both natural and human caused, have their own characteristic scales of influence. The impact of these disturbances and the ensuing ecosystem trajectory depend critically on how the scales of disturbance compare with the scale of connectivity (Allison et al. 2003). Fortunately, new technologies and analytical approaches are at long last opening a window on patterns of movement in the sea.

Tracking movement through parental tags. One potential way to identify the birth site of an individual is through the location of its parents. Parents indelibly mark their offspring with their genes. If enough of the offspring's genotype is known, the identity of potential parents can be evaluated quite rigorously. The problem is that the pool of potential parents is enormous except when offspring dispersal is strictly

limited. If offspring move only a few meters from their parents, the number of candidate parents is small, and paternity can often be established with relative certainty. If offspring can move hundreds of kilometers from their parents, however, identifying paternity is nearly impossible.

Decades ago, population geneticists came up with indirect methods to address this problem (Wright 1948, Felsenstein 1982). Rather than using single individuals to infer patterns of movement, they examined the population-level consequences of movement. Without movement, predictable genetic differences should emerge between geographically isolated subpopulations. As the rate of movement increases, genetic differences decline, especially in genes that are not under selection. The fundamental problem has been that the level of expected geographic difference is large only when migration is quite limited. Even a small rate of migration is sufficient to reduce geographic variation to levels that would be undetectable from sampling noise. As a result, these approaches have been most useful in studying species with limited dispersal potential or in identifying locations where actual movement is far more limited than a simple view of the physics and biology might suggest (Avice 1994, Taylor and Hellberg 2003). From an ecosystem-based management perspective, these constraints are often daunting, since ecologically relevant issues occur across ranges of connectivity where there is little genetic signal.

Emerging conceptual approaches and technological advances are finally breaking through these constraints to provide relevant insight on connectivity for management. The coupling of isolation-by-distance (IBD) models with more explicit models of dispersal through ocean currents (Cowen et al. 2006, Palumbi et al. 2003, Siegel et al. 2003) can greatly increase researchers' ability to detect the signal of connectivity above the inherent noise. Although IBD approaches have their limitations, there are now sufficient data sets to sketch the first tentative pictures of the frequency distribution of coastal marine species' scales of dispersal (Kinlan and Gaines 2003, Kinlan et al. 2005). Other analytical approaches are emerging that may provide estimates of spatial dispersal scales over short time scales (a few years) rather than long-term averages. One promising approach uses Bayesian-based assignment techniques (Corander et al. 2003, Wilson and Rannala 2003, Baudouin et al. 2004), which can provide single-generation estimates of the probability of movement between sampled sites. All of these analytical approaches are greatly aided by enhancements in technology that make it possible to examine far more genes, individuals, and locations than was even conceivable just a few years ago.

Tracking movement through manufactured tags. Animal populations have been studied by tagging and recapturing individuals for well over a century, providing insight into cases of extreme movement when tagged individuals were sighted far from their tagging location. (See Le Cren [1965] for a historical analysis.) Analytical approaches to garner more detailed information on movement have emerged much

more recently (e.g., Turchin and Thoeny 1993, Okubo and Levin 2001, Ovaskainen 2004). Simple markers such as plastic tags, dyes, color bands, bar codes, and rare chemicals are used to artificially tag individuals and track a range of movement statistics. The tags are inexpensive, and the costs of recovery are often borne by others.

Although such tagging studies are providing new insight into animal movement, they have several limitations for studying coastal species. First, they infer patterns of movement statistically rather than document actual paths. Second, they rely on a sizable number of recaptures, which requires either highly efficient recapturing or else marking an enormous number of individuals. Such studies can work well for species that are easily tagged and heavily fished, since there is a high probability that a tagged individual will be caught. By contrast, they offer little benefit for studying large, rare organisms that are difficult to capture and tag initially (e.g., pelagic sharks or tuna) or minute organisms that have high mortality, move large distances, and thus are nearly impossible to recapture (e.g., most larval fish and invertebrates).

The problems of tracking the latter group are unlikely to be resolved with artificial tags (Thorrold et al. 2002), but the challenges of tagging large, highly mobile species have been met head-on by trading cost for intelligence. At modest spatial scales, implanted tags with acoustic signals can be tracked with underwater arrays of sensors to track the location of fish. This helps to define home ranges for relatively sedentary species, to identify habitat preferences and key aggregation sites, and to inform marine reserve design by allowing researchers to estimate the fraction of time fish would most likely be protected within different marine reserve boundaries (e.g., Willis et al. 2001). At much larger spatial scales, computerized tags that can archive data such as the location, physical setting, and even physiological state of tagged individuals, and transmit the information back to shore, are revolutionizing our understanding of the movement of large swimmers (e.g., Boustany et al. 2002, Block et al. 2005). Several cases already show clearly that the scales of current ecosystem and single-species management decisions are at odds with the scales at which organisms move. The most notable case is the demonstration that bluefin tuna regularly cross the international demarcation that purportedly separates independently managed stocks.

Tracking movement through environmental tags. We are likely to wait a long time before archival tags are small enough to track the movement of marine larvae. Depending on the species, larvae can range from tens of microns to a few centimeters in length, and drift in the plankton for as little as a few minutes or more than a year. As we have already noted, artificial tags such as dyes or chemicals also are rarely useful for tracking larvae, since their large potential dispersal scale, coupled with high mortality rates, means that the probability of finding any tagged larvae is remote (but not impossible; see below for new approaches to this problem). A near-ideal solution would be a way to tag all larvae with a

unique marker of their birth site—a “birth certificate” that they must carry with them throughout life, ready to be read by biologists. Even better would be a way to tag the larvae continuously with unique markers of their location as they drift or swim away from their natal site. The combination of a birth certificate and such a larval “flight recorder” (Palumbi et al. 2003, Levin 2006) would definitively resolve the problem of understanding larval connectivity in the sea.

Although no such perfect scenario currently exists, one rapidly advancing approach shares some of these idealized traits. Larvae of fish and some invertebrates produce body parts made of calcium carbonate, which continually grow as the larvae age (e.g., ear bones [otoliths] in fish and statoliths or larval shells in some invertebrates; figure 1). A number of trace elements in seawater can substitute for calcium in the calcium carbonate matrix. If the chemical composition of seawater varies predictably from place to place, the elemental composition of the calcium carbonate that is laid down each day may also vary predictably. Using a mass spectrometer, several studies have now made important inferences about larval origins by reading the chemistry of larval ear bones (Swearer et al. 1999, Thorrold et al. 2002, Zacherl et al. 2003a, 2003b).

For example, Swearer and colleagues (1999) showed that a surprisingly large fraction of fish larvae settling on the coral reefs of St. Croix, US Virgin Islands, actually came from parents on St. Croix. Many larvae were retained close to shore despite their two-month larval life span. Although the island of origin for the remaining immigrant larvae could not be identified, the fact that the majority of larvae were recruited from St. Croix has important implications for management of reef ecosystems on the island. Realizing the dream of this flight-recorder approach, however, has been complicated by a wide range of issues (e.g., temporal variance in water chemistry at a location, small-scale variation in water chemistry, and maternal effects that mask environmental signatures, to name just a few; see Ruttenberg et al. 2005, Warner et al. 2006). Some of these challenges may be resolved by new analytical approaches (e.g., Ben-Tzyi et al. 2007). Others are being addressed by revisiting the challenges of tagging larvae. Larvae can be chemically tagged by exposing them or their parents to compounds not normally found

in nature. If the scale of movement is sufficiently small and the searching sufficiently exhaustive, tagged larvae can be recaptured after marking (Jones et al. 1999, 2005, Almany et al. 2007). Such tagging studies suggest that larvae of many species may not disperse as far from their natal site as previously presumed. This has important implications for the relevant scale of ecosystem management.

Individual performance and health

In terms of ecosystem resilience, a central aspect of an ecosystem's ability to resist and recover from human-induced or natural disturbances is the physiological plasticity and overall health of the resident organisms. The complex relationship between an organism's physiology and health and its environmental conditions is difficult to measure in ecosystems where the interplay between the organism and its environment is very dynamic. However, new tools and approaches are bridging this gap, allowing biologists to understand the condition of organisms in natural populations, and thus their capacity to recover from disturbances, both natural and man-made.

Several new technologies that are being integrated into ecology and management may provide unprecedented insight into the health of organisms in natural populations. Traditional

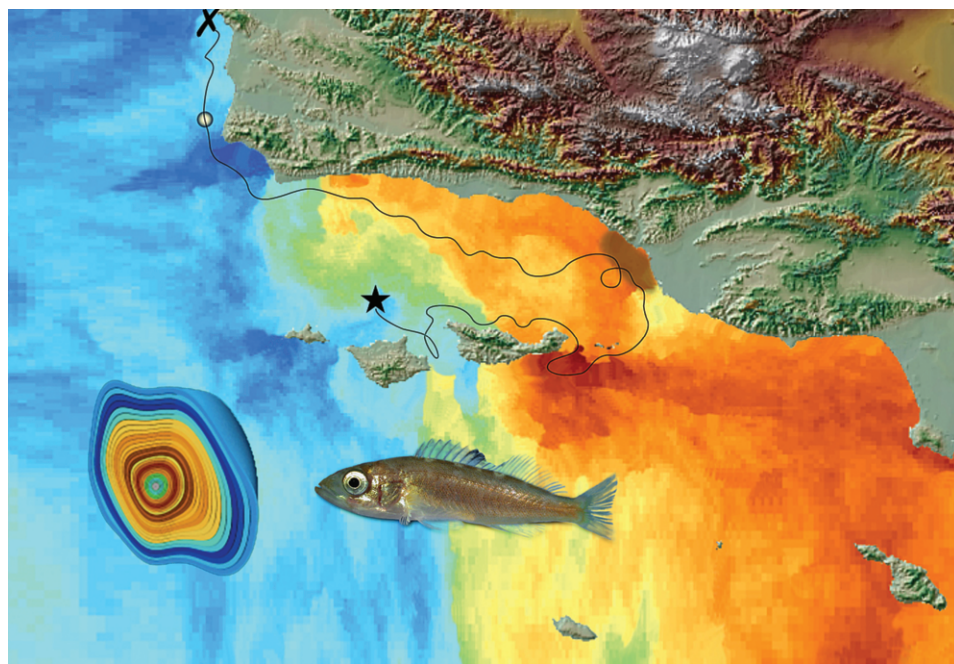


Figure 1. Tracking larvae as they disperse in the sea. Bony structures such as ear bones (otoliths) in fish can carry a record of the travels of larvae as they drift in ocean currents. The chemistry of the bone or shell is altered by the chemistry and physics (temperature, salinity) of the seawater in which it was formed. This image traces the hypothetical path of dispersal of a single larva from its island birth site (marked with a star) to its adult home (marked with an X). The otolith (cross-section inset in lower left) therefore has a permanent chemical record of the larval journey. The daily rings formed in the otolith carry a signal of where they were formed. The question is whether this internal map can be read. The best successes to date have gained insight only on the point of origin, not the path of movement.

assessments of organismal health were observational and limited to the gross detection of such phenomena as abundance, diversity, growth, or the presence of disease. New techniques and approaches are constantly being integrated in the management of ecosystems; examples in this section highlight some hotspots of technology application in critical areas for ecosystem resilience and resistance.

Genomics. Genomics, or the study of organisms and their entire genomes, is ushering in a new era in organismal biology, as biologists gain insight into physiological condition and health as never before (Thomas and Klaper 2004, Hofmann et al. 2005). This field is dependent on large-scale efforts to generate the DNA sequence for all the genes of a particular species. Although the available genetic resources, such as genome sequence databases and DNA libraries, often limit the application of these techniques to model organisms, scientific communities are organizing to overcome this hurdle. For example, the Evolutionary Genomics group at the Joint Genome Institute (www.jgi.doe.gov/whoweare/evogen.html) has recently undertaken the sequencing of coral genomes (Schwarz et al. 2006) as a means to better understand the physiological interplay between the coral host and its endosymbionts, zooxanthellate dinoflagellates. There are also significant efforts to develop genomic resources for other economically important species, including salmon (von Schalburg et al. 2005) and purple sea urchins (Sea Urchin Genome Sequencing Consortium 2006). Overall, the development of genome projects for important species in threatened ecosystems will allow researchers to address more targeted physiological questions using tools that are built on the genomic resources for a particular species. Many of these techniques are already being used in marine systems with great results (Hofmann and Place 2007).

DNA microarrays. The DNA microarray has become central to the pursuit of understanding the response of organisms to the environment (Gracey and Cossins 2003). Microarrays, standard microscope slides with thousands of unique DNA spots on them, are used to quantify the changes in organisms' gene expression. Biological samples containing expressed messenger RNAs (mRNAs) are converted into complementary DNAs and then hybridized to the complementary spots on the microarray. The binding intensity at these spots can then be visualized, and variation in gene expression is quantified and analyzed using bioinformatics tools. Because the profile of gene expression—a representation of genes that are turned off and on—provides a view of the variety of proteins that might be synthesized, changes in gene expression are a representation of how the environment is transduced to the genome. DNA microarrays have been used to analyze the influence of physical factors such as temperature on aquatic organisms (Buckley et al. 2006) and to assess whether individuals within populations vary in patterns of gene expression (Oleksiak et al. 2005). These studies reveal significant changes in gene expression profiles, providing insight into

these study organisms' phenotypic plasticity and perspective on the roles of ecologically significant genes in different environments. Although it is a long journey from the presence of a particular set of mRNAs to whole-animal thermotolerance, these DNA microarray-based studies are illuminating the path to a deeper understanding of how organisms function under variable environmental conditions.

Perhaps no ecosystem better exemplifies the need to understand organismal physiological tolerances than the tropical coral reef. Suffering declines worldwide, coral reefs are thought to be losing viability as a result of coral “bleaching,” a phenomenon in which corals lose their endosymbionts and may never recover. This loss of healthy corals has been shown to shift the ecosystem from coral to algae domination, a situation that may not be highly reversible. Not surprisingly, then, a great deal of importance is placed on understanding the symbiosis between the corals and their endosymbionts in an environmental context. Since the health of corals depends on the relationship of the host with the endosymbionts, and bleaching is thought to be connected to high seawater temperatures or high light levels, understanding the physiological relationship of the coral with the zooxanthellae—and the thermotolerance of this association—is critical to understanding coral health. Future research using DNA microarrays and gene expression profiling (figure 2) will help clarify this relationship and perhaps identify endosymbionts that are “heat specialists.” Recent research on corals has found that a particular strain of the dominant zooxanthellae genus, *Symbiodinium*, tends to be more prevalent in corals that have survived a previous stressful high-temperature bleaching event (Baker et al. 2004). Developing studies on the cnidarian symbioses will contribute to understanding the impacts of global climate change on these important invertebrate species (Rodriguez-Lanetty et al. 2006, Schwarz et al. 2006).

The application of DNA microarrays in ecosystem management holds promise for managing diseases in marine ecosystems and for understanding how organisms might be responding to multiple environmental stressors (Klaper and Thomas 2004). Just as some methods have attempted to find indicators of infection by looking at physiological indices of stress, DNA microarrays stand to provide “physiological fingerprints” of health or disease in individual organisms (Dhar et al. 2003). Such early detection and potential for high throughput of samples could make this technique a major tool for managers to detect outbreaks in their systems.

Co-opting engineering technology to measure the body temperature of marine animals. To understand an organism's response to disturbance and its capacity to recover from stress, it is necessary to have information about how the environment affects the performance and physiology of the organism. New technologies that take advantage of miniaturized electronics and microprocessor-based data loggers are being deployed to collect real-time, ecologically relevant data about such things as body temperature in animals while they move about and interact with their environment. For exam-

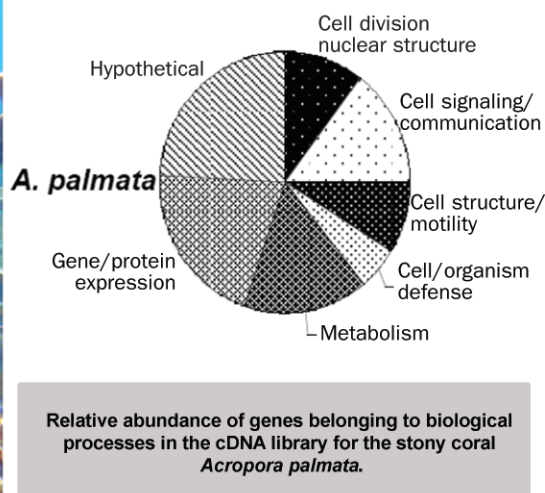


Figure 2. Coral genomics has the potential to provide unprecedented insight into the nature of the symbiosis between corals and their endosymbionts. Recent efforts to sequence the genome of corals such as *Acropora* species have cataloged thousands of individual genes, all of which are distributed among various cellular processes of the organism. This sequence information can then be used to perform studies that address the physiology of corals and the mechanisms that maintain and support the symbiotic relationship of the corals with their algal symbionts. Photograph and graphic courtesy of Mónica Medina, University of California–Merced.

ple, many satellite tags that are deployed on Pacific pelagics collect seawater and body temperature, giving scientists clues about how these organisms select water temperature.

In marine coastal ecosystems, intertidal mussels—sessile invertebrates found in large, dense beds on outer rocky shores—have emerged as important sentinel organisms in the study of animals' response to their thermal environment (figure 3). Using small data loggers, marine ecologists have been measuring mussel body temperatures, linking these changes in body temperature to physiological changes in the animal, and profiling the body temperature of mussel populations at different latitudes on the western coast of the United States (Helmuth et al. 2002). There, studies of the mussel body temperatures are being used to link local climate to organismal performance as a means to predict the impact of climate change on natural populations. Because the intertidal zone is subject to alternating aquatic and terrestrial conditions caused by the movement of the tides, the resident organ-

isms must be tolerant of extremely high temperatures when they are out of the water, a stress that will increase with warming of local climate. In these vulnerable coastal marine ecosystems (Harley et al. 2006), intertidal organisms such as the California mussel may be the “canary in the coal mine” in the context of global climate change (Helmuth et al. 2002).

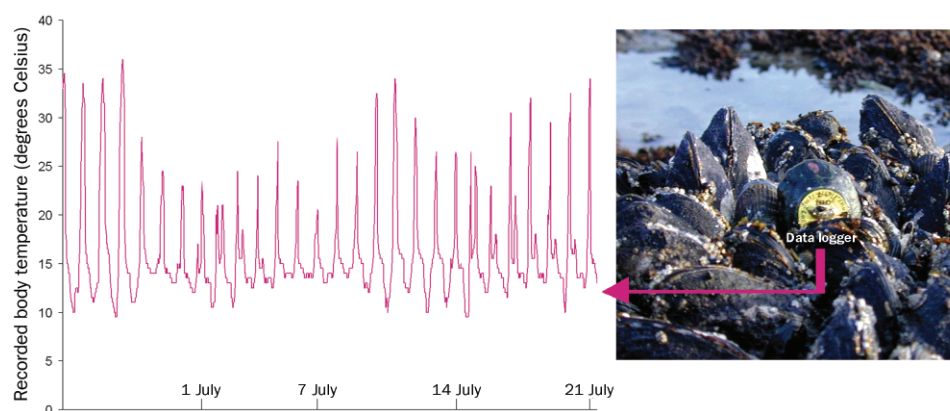


Figure 3. Small data loggers set in epoxy, formed in the shape of mussel shells, have provided unique data about organismal body temperature and how this organismal trait is driven by local weather patterns (Helmuth et al. 2002). This integration of technology has the potential to “scale up” where the mussels are indicator organisms for the impact of climate change on large spatial scales. Image courtesy of Brian Helmuth.

Remote sensing as an ecosystem management tool. Often, the information requirements for effective management are not met by assessing health on small spatial scales—that is, by looking at single populations or at the gene expression of a few individuals. Remote-sensing technologies and the integration of satellite-based data into management strategies are facilitating studies of ecosystem status over large areas in coral reef ecosystems. While remote-sensing technology has been integrated into coral reef management in many ways, one significant goal is to gather data regarding coral cover and the extent of bleaching over large areas. Recently, advances in spectral analysis (e.g., higher-resolution and multispectral images) have allowed for the differentiation of live and bleached corals because the bleached corals are brighter in the visible spectra (Mumby et al. 2001). Although these results represent a significant advance, their accuracy is debated because of effects that interfere with satellite imagery, such as the variable optical qualities of the water column (Elvidge et al. 2004). Other remote-sensing databases have been used to detect coral spawning as a result of insolation (Penland et al. 2004). Being able to predict bleaching events is a capacity that, although it does not monitor coral health immediately, assists managers in gaining a perspective on upcoming stresses to their area. Elevated sea-surface temperatures (SSTs) have been strongly correlated to bleaching events, and recent analyses have examined the characteristics of SSTs that are most closely linked to bleaching events (Berkelmans et al. 2004). At a more organized level, the National Oceanic and Atmospheric Administration and the Coral Reef Watch program have released a satellite image-based tool that employs a cumulative metric of heat stress to corals (degree heating weeks) as a risk-analysis resource for coral reef managers to help predict the risk of a bleaching event, given a level of accumulated stress experienced by corals in their reefs (www.osdpd.noaa.gov/PSB/EPS/SST/dhw_retro.html). These remote-sensing technologies will contribute significantly to management efforts and foster rapid, large-scale assessments of ecosystem health in coral reefs.

Conclusions

As one step toward the implementation of ecosystem-based management in the oceans is to understand the nature of healthy marine ecosystems (Ruckelshaus et al. 2008), the tools described here will contribute information about the health and abundance of resident organisms. In addition, tools such as these may assist in setting standards to assess the outcome of management decisions. Finally, given the complexity of managing marine ecosystems in the face of potentially interacting stressors, the need to assess the health of marine ecosystems is increasing. As processes such as global climate change (Harley et al. 2006), ocean acidification (Kleypas et al. 2006), and the loss of biodiversity (Parmesan 2006) act on marine ecosystems, the tools that allow managers to count and assess the health of the organisms in an ecosystem will contribute significantly to the development of effective management strategies in the future.

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